

**COMPARATIVE ANALYSIS OF NUCLEIC ACIDS USING  
POPULATION TAGGING**

**ABSTRACT**

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Disclosed are methods that allow one or more nucleic acid targets to be compared across two or more nucleic acid samples. Nucleic acid tags are appended to the samples to be assessed, such that each sample has a unique tag. The tagged nucleic acids are then mixed, and the targets within the mixture are amplified. The amplification products are distinguished using the unique tag domains to reveal the abundance of the amplification products derived from each sample, which correlates to the relative abundance of the target in the samples.

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